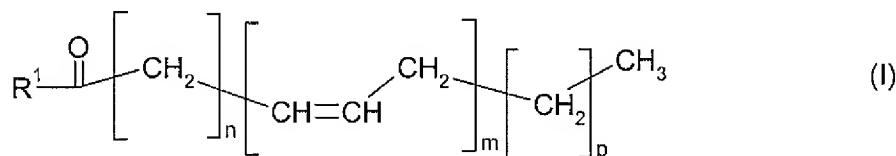


AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A process for the production of compounds of the general formula I

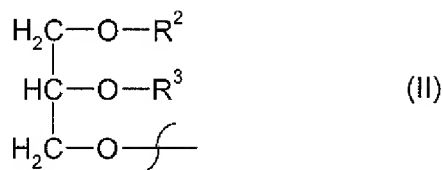


in the seed of transgenic plants with a content of at least 20% by weight based on the total lipid content, which comprises the following process steps:

- a) introducing, into the organism, at least one nucleic acid sequence which encodes a $\Delta 9$ -elongase or $\Delta 6$ -desaturase activity, and
- b) introducing, into the organism, at least one nucleic acid sequence which encodes a $\Delta 8$ -desaturase or $\Delta 6$ -elongase activity, and
- c) introducing, into the organism, at least one nucleic acid sequence which encodes a $\Delta 5$ -desaturase activity, and
- d) introducing, into the organism, at least one nucleic acid sequence which encodes a $\Delta 5$ -elongase activity, and
- e) introducing, into the organism, at least one nucleic acid sequence which encodes a $\Delta 4$ -desaturase activity, and

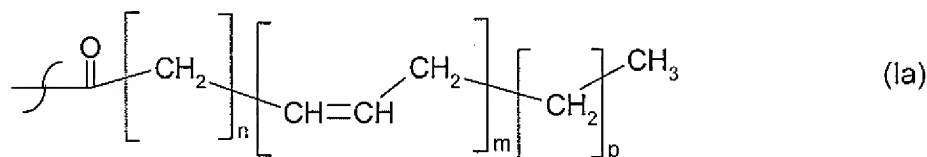
where the variables and substituents in formula I have the following meanings:

$\text{R}^1 =$ hydroxyl, coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the general formula II



R^2 = hydrogen, lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated C_2 - C_{24} -alkylcarbonyl,

R^3 = hydrogen, saturated or unsaturated C_2 - C_{24} -alkylcarbonyl, or R^2 and R^3 independently of one another are a radical of the general formula Ia:



in which

$n = 2, 3, 4, 5, 6, 7$ or 9 , $m = 2, 3, 4, 5$ or 6 and $p = 0$ or 3 .

2. (Original) The process according to claim 1, wherein the variables n , m and p have the following meanings:

$n = 2, 3$ or 5 , $m = 4, 5$ or 6 and $p = 0$ or 3 .

3. (Previously presented) The process according to claim 1, wherein, in formula I, the variables n , m and p have the following meanings:

- (a) $m = 4$, $n = 3$, $p = 3$ and the compound is arachidonic acid,
- (b) $m = 5$, $n = 3$, $p = 0$ and the compound is eicosapentaenoic acid,
- (c) $m = 5$, $n = 5$, $p = 0$ and the compound is docosapentaenoic acid, or
- (d) $m = 6$, $n = 3$, $p = 0$ and the compound is docosahexaenoic acid.

4. (Previously presented) The process according to claim 2, wherein, in the seed of the transgenic plant, the content of all compounds of the formula I together amounts to at least 27% by weight based on the total lipid content.

5. (Previously presented) The process according to claim 3, wherein, in the seed of the transgenic plant, the docosahexaenoic acid content amounts to at least 1% by weight based on the total lipid content.
6. (Currently amended) The process according to claim 1, wherein the nucleic acid sequences which encode polypeptides with ~~$\Delta 9$ -elongase~~, $\Delta 6$ -desaturase, ~~$\Delta 8$ -desaturase~~, $\Delta 6$ -elongase, $\Delta 5$ -desaturase, $\Delta 5$ -elongase or $\Delta 4$ -desaturase activity are selected from the group consisting of
 - a) a nucleic acid sequence with the sequence shown in ~~SEQ ID NO: 1~~, ~~SEQ ID NO: 3~~, ~~SEQ ID NO: 5~~, ~~SEQ ID NO: 7~~, ~~SEQ ID NO: 9~~, ~~SEQ ID NO: 11~~, ~~SEQ ID NO: 13~~, ~~SEQ ID NO: 15~~, ~~SEQ ID NO: 17~~, ~~SEQ ID NO: 19~~, ~~SEQ ID NO: 21~~, ~~SEQ ID NO: 23~~, ~~SEQ ID NO: 25~~, ~~SEQ ID NO: 27~~, ~~SEQ ID NO: 29~~, ~~SEQ ID NO: 31~~, ~~SEQ ID NO: 33~~, ~~SEQ ID NO: 35~~, ~~SEQ ID NO: 37~~, ~~SEQ ID NO: 39~~, ~~SEQ ID NO: 41~~, ~~SEQ ID NO: 43~~, ~~SEQ ID NO: 45~~, ~~SEQ ID NO: 47~~, ~~SEQ ID NO: 49~~, ~~SEQ ID NO: 51~~, ~~SEQ ID NO: 53~~, ~~SEQ ID NO: 59~~, ~~SEQ ID NO: 61~~, ~~SEQ ID NO: 63~~, ~~SEQ ID NO: 65~~, ~~SEQ ID NO: 67~~, ~~SEQ ID NO: 69~~, ~~SEQ ID NO: 71~~, ~~SEQ ID NO: 73~~, ~~SEQ ID NO: 75~~, ~~SEQ ID NO: 77~~, ~~SEQ ID NO: 79~~, ~~SEQ ID NO: 81~~, ~~SEQ ID NO: 83~~, ~~SEQ ID NO: 85~~, ~~SEQ ID NO: 89~~, ~~SEQ ID NO: 91~~, ~~SEQ ID NO: 93~~, ~~SEQ ID NO: 95~~, ~~SEQ ID NO: 97~~, ~~SEQ ID NO: 99~~, ~~SEQ ID NO: 101~~, ~~SEQ ID NO: 103~~, ~~SEQ ID NO: 111~~, ~~SEQ ID NO: 113~~, ~~SEQ ID NO: 117~~, ~~SEQ ID NO: 119~~, ~~SEQ ID NO: 131~~, ~~SEQ ID NO: 133~~, ~~SEQ ID NO: 135~~, ~~SEQ ID NO: 137~~, ~~SEQ ID NO: 183~~, ~~SEQ ID NO: 193~~, ~~SEQ ID NO: 197~~, ~~SEQ ID NO: 199~~ or ~~SEQ ID NO: 201~~, or
 - b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequences shown in ~~SEQ ID NO: 2~~, ~~SEQ ID NO: 4~~, ~~SEQ ID NO: 6~~, ~~SEQ ID NO: 8~~, ~~SEQ ID NO: 10~~, ~~SEQ ID NO: 12~~, ~~SEQ ID NO: 14~~, ~~SEQ ID NO: 16~~, ~~SEQ ID NO: 18~~, ~~SEQ ID NO: 20~~, ~~SEQ ID NO: 22~~, ~~SEQ ID NO: 24~~, ~~SEQ ID NO: 26~~, ~~SEQ ID NO: 28~~, ~~SEQ ID NO: 30~~, ~~SEQ ID NO: 32~~, ~~SEQ ID NO: 34~~, ~~SEQ ID NO: 36~~, ~~SEQ ID NO: 38~~, ~~SEQ ID NO: 40~~, ~~SEQ ID NO: 42~~, ~~SEQ ID NO: 44~~, ~~SEQ ID NO: 46~~, ~~SEQ ID NO: 48~~, ~~SEQ ID NO: 50~~, ~~SEQ ID NO: 52~~, ~~SEQ ID NO: 54~~, ~~SEQ ID NO: 60~~, ~~SEQ ID NO: 62~~, ~~SEQ ID NO:~~

~~64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202, or and~~

- c) derivatives of the nucleic acid sequence shown in ~~SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201,~~ which encode polypeptides with at least 40% identity at the amino acid level with ~~SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70,~~

~~SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202~~ and which have ~~$\Delta 9$ -elongase~~, $\Delta 6$ -desaturase, $\Delta 8$ -desaturase, $\Delta 6$ -elongase, $\Delta 5$ -desaturase, $\Delta 5$ -elongase or $\Delta 4$ -desaturase activity.

7. (Previously presented) The process according to claim 1, wherein a nucleic acid sequence which encodes polypeptides with $\omega 3$ -desaturase activity, selected from the group consisting of:
 - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, or
 - b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 88 or SEQ ID NO: 106, or
 - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 88 or SEQ ID NO: 106 and which have $\omega 3$ -desaturase activityis additionally introduced into the transgenic plant.
8. (Previously presented) The process according to claim 1, wherein a nucleic acid sequence which encodes polypeptides with $\Delta 12$ -desaturase activity, selected from the group consisting of:
 - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, or
 - b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 108, SEQ ID

NO: 110 or SEQ ID NO: 196, or

- c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196 and which have $\Delta 12$ -desaturase activity

is additionally introduced into the transgenic plant.

9. (Previously presented) The process according to claim 1, wherein a nucleic acid sequence which encodes proteins of the biosynthetic pathway of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s) is additionally introduced into the transgenic plant.
10. (Previously presented) The process according to claim 1, wherein the substituents R^2 or R^3 independently of one another are saturated or unsaturated C_{18} - C_{22} -alkylcarbonyl.
11. (Previously presented) The process according to claim 1, wherein the substituents R^2 or R^3 independently of one another are unsaturated C_{18} -, C_{20} - or C_{22} -alkylcarbonyl with at least two double bonds.
12. (Previously presented) The process according to claim 1, wherein the transgenic plant is selected from the group consisting of an oil-producing plant, a vegetable plant and an ornamental.
13. (Previously presented) The process according to claim 1, wherein the transgenic plant is selected from the group of the plant families consisting of:
- Anacardiaceae, Asteraceae, Boraginaceae, Brassicaceae, Cannabaceae, Compositae, Cruciferae, Cucurbitaceae, Elaeagnaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Leguminosae, Linaceae, Malvaceae, Moringaceae, Marchantiaceae,

Onagraceae, Olacaceae, Oleaceae, Papaveraceae, Piperaceae, Pedaliaceae, Poaceae and Solanaceae.

14. (Previously presented) The process according to claim 1, wherein the compounds of the general formula I are isolated from the transgenic plant in the form of their oils, lipids or free fatty acids.
15. (Previously presented) A process for the production, in transgenic plants, of compounds of the general formula I according to claim 1, comprising:
 - a) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a $\Delta 6$ -desaturase activity and is selected from the group consisting of:
 - i) a nucleic acid sequence with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201,
 - ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 194 or SEQ ID NO: 202,
 - iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201, and
 - iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201,
 - b) introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with a $\Delta 6$ -elongase activity and is selected from the group consisting of:
 - i) a nucleic acid sequence with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199,
 - ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 28 or SEQ ID NO: 200,
 - iii) nucleic acid sequences which hybridize under stringent conditions with

the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199, and

- iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199, and
- c) introducing, into the plant, at least one nucleic acid sequence which encodes a polypeptide with a $\Delta 5$ -desaturase activity and is selected from the group consisting of:
 - i) a nucleic acid sequence with the sequence shown in SEQ ID NO: 11,
 - ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 12,
 - iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 11, and
 - iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 11,

where the variables and substituents in formula I have the meaning given in claim 1.

- 16. (Original) The process according to claim 15, where the substituents R^2 or R^3 independently of one another are saturated or unsaturated C_{10} - C_{22} -alkylcarbonyl.
- 17. (Previously presented) The process according to claim 15, wherein the substituents R^2 or R^3 independently of one another are unsaturated C_{18} -, C_{20} - or C_{22} -alkylcarbonyl with at least two double bonds.
- 18. (Previously presented) The process according to claim 15, wherein a nucleic acid sequence which encodes a polypeptide with a $\Delta 12$ -desaturase activity is additionally introduced into the plant.
- 19. (Original) The process according to claim 18, wherein the nucleic acid sequence is selected from the group consisting of:
 - a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 195,

- b) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 196,
 - c) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 195, and
 - d) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 195.
20. (Original) The process according to claim 18, wherein the $\Delta 12$ -desaturase is expressed under the control of a seed-specific promoter.
21. (Previously presented) The process according to claim 15, wherein a nucleic acid sequence which encodes a polypeptide with a $\Delta 5$ -elongase activity is additionally introduced into the plant.
22. (Original) The process according to claim 21, wherein the nucleic acid sequence is selected from the group consisting of:
- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197,
 - b) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 44, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 86, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138 or SEQ ID NO: 198,
 - c) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 43,

SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197, and

- d) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197.
23. (Original) The process according to claim 21, wherein the $\Delta 5$ -elongase is expressed under the control of a seed-specific promoter.
24. (Previously presented) The process according to claim 15, wherein all nucleic acid sequences are introduced into the plants on a shared recombinant nucleic acid molecule.
25. (Original) The process according to claim 24, wherein each nucleic acid sequence is under the control of its own promoter.
26. (Original) The process according to claim 25, wherein the own promoter is a seed-specific promoter.
27. (Previously presented) The process according to claim 15, wherein, in formula I, the variables n, m and p have the following meanings:
- (a) $m = 4$, $n = 3$, $p = 3$ and the compound is arachidonic acid,
- (b) $m = 5$, $n = 3$, $p = 0$ and the compound is eicosapentaenoic acid, or
- (c) $m = 6$, $n = 3$, $p = 0$ and the compound is docosahexanoic acid.
28. (Previously presented) The process according to claim 15, wherein the plant is an oil seed plant or oil fruit plant.

29. (Original) The process according to claim 28, wherein the plant is selected from the group consisting of soybean, peanut, oilseed rape, canola, linseed, evening primrose, mullein, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut and coconut.
30. (Previously presented) The process according to claim 28, wherein the plant is *Brassica juncea*.
31. (Previously presented) The process according to claim 15, wherein the compounds of the formula I are obtained from the plant in the form of their oils, lipids and free fatty acids.
32. (Original) The process according to claim 31, wherein unsaturated or saturated fatty acids are liberated from the compounds of the formula I.
33. (Original) The process according to claim 32, wherein the liberation is effected by alkaline hydrolysis or enzymatic cleavage.
34. (Previously presented) The process according to claim 27, wherein the arachidonic acid concentration amounts to at least 25% based on the total lipid content of the transgenic plant.
35. (Previously presented) The process according to claim 27, wherein the eicosapentaenoic acid concentration amounts to at least 15% based on the total lipid content of the transgenic plant.
36. (Previously presented) An oil, lipid or fatty acid or a fraction thereof, obtained by the process according to claim 1.
37. (Cancelled)
38. (Original) A recombinant nucleic acid molecule comprising:
 - a) one or more copies of a promoter which is active in plant cells, preferably in seed cells,
 - b) at least one nucleic acid sequence as defined in claim 15 which encodes a $\Delta 6$ -desaturase activity,

- c) at least one nucleic acid sequence as defined in claim 15 which encodes a $\Delta 5$ -desaturase activity,
 - d) at least one nucleic acid sequence as defined in claim 15 which encodes a $\Delta 6$ -elongase activity, and
 - e) one or more copies of a terminator sequence.
39. (Previously presented) The recombinant nucleic acid molecule according to claim 38, additionally comprising a nucleic acid sequence which encodes a polypeptide with $\Delta 12$ -desaturase activity.
40. (Previously presented) The recombinant nucleic acid molecule according to claim 38, additionally comprising a nucleic acid sequence which encodes a polypeptide with $\Delta 5$ -elongase activity.
41. (Previously presented) The recombinant nucleic acid molecule according to claim 38, additionally comprising biosynthesis genes of the fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases and fatty acid elongase(s).
42. (Previously presented) The recombinant nucleic acid molecule according to claim 38, additionally comprising biosynthesis genes of the fatty acid or lipid metabolism, selected from the group consisting of $\Delta 4$ -desaturase, $\Delta 8$ -desaturase, $\Delta 9$ -desaturase or $\Delta 9$ -elongase.
43. (Previously presented) A transgenic plant comprising a the recombinant nucleic acid molecule according to claim 38.
44. (Previously presented) The process according to claim 15, wherein the compounds of the general formula I are isolated from the transgenic plant in the form of their oils, lipids or free fatty acids.
45. (Previously presented) An oil, lipid or fatty acid or a fraction thereof, produced by the

process according to claim 15.

46. (Previously presented) An oil, lipid or fatty acid composition which comprises PUFAs produced by the process according to claim 1 and which is derived from the transgenic plants.
47. (Previously presented) A process for the production of oils, lipids or fatty acid compositions by mixing the oil, lipid or fatty acid compositions according to claim 46 with animal or microbial oils, lipids or fatty acids.
48. (Previously presented) Feed, foodstuffs, cosmetics or pharmaceuticals prepared from the oil, lipid or fatty acid compositions according to claim 46.
49. (Original) An isolated nucleic acid sequence which encodes polypeptides with $\Delta 5$ -elongase activity and which has the sequence shown in SEQ ID NO: 197.
50. (Original) An isolated nucleic acid sequence which encodes polypeptides with $\Delta 6$ -elongase activity and which has the sequence shown in SEQ ID NO: 199.
51. (Original) An isolated nucleic acid sequence which encodes polypeptides with $\Delta 6$ -desaturase activity and which has the sequence shown in SEQ ID NO: 201.
52. (Previously presented) A gene construct comprising ~~an~~ the isolated nucleic acid according to claim 49, wherein the nucleic acid is linked functionally to one or more regulatory signals.
53. (Previously presented) The gene construct according to claim 52, wherein the nucleic acid construct comprises additional biosynthesis genes of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s).
54. (Previously presented) A vector comprising the isolated nucleic acid according to claim 50.

55. (Previously presented) A transgenic plant comprising at least one nucleic acid according to claim 50.
56. (Previously presented) A gene construct comprising the isolated nucleic acid according to claim 50, wherein the nucleic acid is linked functionally to one or more regulatory signals.
57. (Previously presented) A gene construct comprising the isolated nucleic acid according to claim 51, wherein the nucleic acid is linked functionally to one or more regulatory signals.
58. (Previously presented) The gene construct according to claim 56, wherein the nucleic acid construct comprises additional biosynthesis genes of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s).
59. (Previously presented) The gene construct according to claim 57, wherein the nucleic acid construct comprises additional biosynthesis genes of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s).
60. (Previously presented) A vector comprising the isolated nucleic acid according to claim 51.
61. (Previously presented) A vector comprising the gene construct according to claim 52.
62. (Previously presented) A transgenic plant comprising at least one nucleic acid according to claim 51.

63. (Previously presented) A transgenic plant comprising at least one gene construct according to claim 52.